

SEQUENCE LISTING

<110> Hitz, William
 Sebastian, Scott
 Grace, John
 Streit, Leon

<120> SOYBEAN PLANT PRODUCING SEEDS WITH REDUCED LEVELS OF RAFFINOSE
 SACCHARIDES AND PHYTIC ACID

<130> BB-1077-C

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<150> 08/835,751
 <151> APRIL 8, 1997

<150> PCT/US98/06822
 <151> APRIL 7, 1998

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<400> 2

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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45
Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
50 55 60
Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
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85 90 95
Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
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Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
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Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140
Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160
Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
165 170 175
Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
180 185 190
Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
195 200 205
Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
210 215 220
Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225 230 235 240
Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
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Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270
Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
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Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
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Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
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Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
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His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
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 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
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 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
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 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
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 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
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 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
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 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

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<210> 4
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

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<210> 5
 <211> 1533
 <212> DNA
 <213> Glycine max

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 aaattagggg taatgcttgt gggttggggg ggaaacaacg gctcaaccct caccggtggt 240
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<210> 6
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<212> PRT
<213> Glycine max

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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
  35             40             45

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
  50             55             60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
  65             70             75             80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
      85             90             95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
  100            105            110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
  115            120            125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
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Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
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Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
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Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

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<210> 9
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<212> PRT
<213> Glycine max

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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45
Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
50 55 60

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Val	Gly	Ser 115	Phe	Gln	Gly	Glu	Glu 120	Ile	Tyr	Ala	Pro	Phe 125	Lys	Ser	Leu
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Val 385	Ile	Lys	Tyr	Val	Pro 390	Tyr	Val	Gly	Asp	Ser 395	Lys	Arg	Ala	Met	Asp 400
Glu	Tyr	Thr	Ser	Glu 405	Ile	Phe	Met	Gly	Gly 410	Lys	Ser	Thr	Ile	Val 415	Leu

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
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Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

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<212> PRT
<213> Glycine max

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20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val	Asn	Tyr	Gln	Phe	Lys	Thr	Asn	Thr	His	Val	Pro	Lys	Leu	Gly	Val	50	55	60
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Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn	325	330	335
His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	Thr	Phe	340	345	350
Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Asn	Val	Val	Asp	Asp	Met	Val	Asn	355	360	365
Ser	Asn	Ala	Ile	Leu	Tyr	Glu	Pro	Gly	Glu	His	Pro	Asp	His	Val	Val	370	375	380
Val	Ile	Lys	Tyr	Val	Pro	Tyr	Val	Gly	Asp	Ser	Lys	Arg	Ala	Met	Asp	385	390	395

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
 405 410 415
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
 420 425 430
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
 435 440 445
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
 465 470 475 480
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
 485 490 495
 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
 500 505 510

<210> 13
 <211> 1533
 <212> DNA
 <213> Glycine max

<400> 13
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 cagtggattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca 180
 aaattggggg tgatgcttgt ggggttgggt ggaaacaacg gctctaccct caccggtggt 240
 gttattgcta acagagaggg catttcattg gctacaaagg acaagattca acaagccaat 300
 tactttggct cctcaccoca agcctcagct attcgagttg gatccttcca gggagaggaa 360
 atctatgccc cattcaagag tctgcttcca atggttaatc ctgacgacat tgtgtttggg 420
 ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac 480
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 tacgaccggg atttcattgc tgccaaccaa gaggagcgtg ccaacaacgt gattaagggc 600
 acaaagcaag agcaagttca gcaaatcatc aaagacatca aggcgtttta ggaagccacc 660
 aaagtggaca aggtggttgt cctgtggact gccaacacag agaggtatag caatttgggt 720
 gtaggcctta atgacacat ggagaatctc ttggctgctg tggacagaaa tgaggctgag 780
 atttctcctt ccaccttgta tgccattgcc tgtgtgatgg aaaatgttcc tttcattaat 840
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 accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtgggtgaat 1440
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 ccagagaata acatgattct cgagtacaag tga 1533

<210> 14
 <211> 510
 <212> PRT
 <213> Glycine max

<400> 14
 Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
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 Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
 20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
 35 40 45
 Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
 50 55 60
 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
 65 70 75 80
 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
 85 90 95
 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
 100 105 110
 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
 115 120 125
 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
 130 135 140
 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
 145 150 155 160
 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
 165 170 175
 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
 180 185 190
 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
 195 200 205
 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
 210 215 220
 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
 225 230 235 240
 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
 245 250 255
 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
 260 265 270
 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
 275 280 285
 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
 290 295 300
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
 305 310 315 320
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
 325 330 335
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
 370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 15
<211> 1533
<212> DNA
<213> Glycine max

<400> 15
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cagtggtattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca 180
aaattggggg tgatgcttgt ggggttggggg ggaacaacg gctctaccct caccggtggt 240
gttattgcta acagagaggg catttcattg gctacaaagg acaagattca acaagccaat 300
tactttggct ccctcaccca agcctcagct attcgagttg gatccttcca gggagaggaa 360
atctatgccc cattcaagag tctgcttcca atgggttaatc ctgacgacat tgtgtttggg 420
ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac 480
atcgatttgc agaagcagtt gaggccttac atggaatcca tggttccact ccccggaatc 540
tacgaccggg atttcattgc tgccaaccaa gaggagcgtg ccaacaacgt gattaagggc 600
acaaagcaag agcaagttca gcaaatcatc aaagacatca aggcgtttta ggaagccacc 660
aaagtggaca aggtggttgt cctgtggact gccaaacacag agaggtatag caatttggtt 720
gtaggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag 780
atttctcctt ccaccttcta tgccattgcc tgtgtgatgg aaaatgttcc ttccattaat 840
ggaagccctc agaacacttt tgtaccaggg ctgattgac ttgccatgc gaggaacact 900
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aacgttggtt acgatattgt caacagcaat gccatcctct atgagcctgg tgaacatccc 1140
gaccatgttg ttgtatttaa gtatgtgcct tacgtagggg atagcaagag agccatggat 1200
gagtacactt cagagatatt catgggtgga aagaacacca ttgttttgca caacacatgt 1260
gaggattccc ttttagctgc tctattatc ttggacttgg tcttcttgc tgagctgagc 1320
actagaatcc agtttaaagc tgaaaatgag ggaatttcc actcattcca cccagttgct 1380
accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtgggtgaat 1440
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ccagagaata acatgattct cgagtacaag tga 1533

<210> 16
<211> 510
<212> PRT
<213> Glycine max

<400> 16
Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
 20 25 30
 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
 35 40 45
 Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
 50 55 60
 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
 65 70 75 80
 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
 85 90 95
 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
 100 105 110
 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
 115 120 125
 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
 130 135 140
 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
 145 150 155 160
 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
 165 170 175
 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
 180 185 190
 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
 195 200 205
 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
 210 215 220
 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
 225 230 235 240
 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
 245 250 255
 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
 260 265 270
 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
 275 280 285
 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
 290 295 300
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
 305 310 315 320
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
 325 330 335
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
 370 375 380
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
 385 390 395 400
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
 405 410 415
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
 420 425 430
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
 435 440 445
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
 465 470 475 480
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
 485 490 495
 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
 500 505 510